

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/550,758
Source: PUS/10
Date Processed by STIC: 10/7/05

ENTERED



PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/550,758

DATE: 10/07/2005
TIME: 09:29:19

Input Set : A:\58049-00019.ST25.txt
Output Set: N:\CRF4\10072005\J550758.raw

2 <110> APPLICANT: Republic of National Fisheries Research and Development Institute
 3 KIM, Young Ok
 4 KIM, Han Woo
 5 LEE, Jeong Ho
 6 KIM, Kyung Kil
 7 LEE, Jong Yun
 8 KONG, In Soo
 10 <120> TITLE OF INVENTION: Phytase produced from Citrobacter braakii
 12 <130> FILE REFERENCE: 58049-00019
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/550,758
 C--> 14 <141> CURRENT FILING DATE: 2005-09-23
 14 <150> PRIOR APPLICATION NUMBER: PCT/KR2004/000680
 15 <151> PRIOR FILING DATE: 2004-03-25
 17 <150> PRIOR APPLICATION NUMBER: KR 10-2003-0018573
 18 <151> PRIOR FILING DATE: 2003-03-25
 20 <160> NUMBER OF SEQ ID NOS: 8
 22 <170> SOFTWARE: KopatentIn 1.71
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 1481
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Citrobacter braakii YH-15
 29 <220> FEATURE:
 30 <221> NAME/KEY: MISC_FEATURE
 31 <222> LOCATION: (1134)..(1134)
 32 <223> OTHER INFORMATION: n can be a, c, g or t
 34 <400> SEQUENCE: 1
 35 tagagtttga tcctggctca gattgaacgc tggcggcagg cctaacacat gcaagtcgaa 60
 37 cggtagcaca gaggagctt ctccttgggt gacgagtggc ggacgggtga gtaatgtctg 120
 39 ggaaaactgcc cgatggaggg ggataactac tggaaacggg agctaataacc gcataacgtc 180
 41 gcaagaccaa agagggggac cttcgggcct cttgcacatcg gatgtgcca gatgggatta 240
 43 gcttagtaggt ggggtaacgg ctcacacctt cgacgatccc tagctggct gagaggatga 300
 45 ccagccacac tggaaactgag acacggtcca gactcctacg ggaggcagca gtggggata 360
 47 ttgcacaatg ggcgcaagcc ttagtgcagcc atgcccgtg tatgaagaag gccttcgggt 420
 49 tgtaaagtac ttccagcggag gaggaaagggt ttgtgtttaa taaccgcagc aattgacgtt 480
 51 actcgcagaa gaagcaccgg ctaactccgt gccagcagcc gcggtaataac ggagggtgca 540
 53 agcgttaatc ggaattactg ggcttaaagc gcacgcaggc ggtctgtcaa gtctggatgt 600
 55 aaatccccgg gctcaacctg ggaactgcat ccgaaactgg caggctagag tcttgtagag 660
 57 gggggtagaa ttccaggtgt agcgggtgaaa tgcgttagaga tctggaggaa taccgggtggc 720
 59 gaaggcggcc ccctggacaa agactgacgc tcaggtgcga aagcgtgggg agcaaacagg 780
 61 attagataacc ctggtagtcc acggcgtaaa cgatgtcgac ttggaggtt tgcccttgag 840
 63 gcgtggcttc cggagctaac gcgttaagtc gaccgcctgg ggagtacggc cgcaagggtt 900
 65 aaactcaaat gaattgacgg gggccccgac aagcggtgga gcatgtgggtt taattcgatg 960
 67 caacgcgaag aaccttaccc actcttgaca tccagagaac ttagcagaga tgctttgggt 1020

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69 ccttcggaa ctctgagaca ggtgctgcat ggctgtcgac agctcgtgtt gtgaaatgtt 1080
W--> 71 gggtaagtc ccgcaacgag cgcaaccctt atcccttggtt gccagcggtt cggncggaa 1140
 73 ctc当地aggag actgccagtg ataaaactgga ggaagggtggg gatgacgtca agtcatcatg 1200
 75 gccc当地tacga gtagggctac acacgtgcta caatgcata tacaaaagaga agc当地acctcg 1260
 77 cgagagcaag cggacccat aaagtatgtc gtagtccgga ttggagtc当地g caactcgact 1320
 79 ccatgaagtc ggaatcgcta gtaatcgtgg atc当地aatgc cacggtaat acgttccc当地g 1380
 81 gc当地tgtaca caccgccc当地t cacaccatgg gagtgggttg caaaagaagt aggtagctt 1440
 83 accttc当地gga gggcgcttac ctctttggat tc当地atgggg a 1481
 86 <210> SEQ ID NO: 2
 87 <211> LENGTH: 10
 88 <212> TYPE: PRT
 89 <213> ORGANISM: Citrobacter braakii YH-15
 91 <400> SEQUENCE: 2
 92 Glu Glu Gln Asn Gly Met Lys Leu Glu Arg
 93 1 5 10
 96 <210> SEQ ID NO: 3
 97 <211> LENGTH: 12
 98 <212> TYPE: PRT
 99 <213> ORGANISM: Escherichia coli
 101 <400> SEQUENCE: 3
 102 Ser Glu Pro Glu Leu Lys Leu Glu Asn Ala Val Val
 103 1 5 10
 106 <210> SEQ ID NO: 4
 107 <211> LENGTH: 15
 108 <212> TYPE: PRT
 109 <213> ORGANISM: Aspergillus ficuum
 111 <400> SEQUENCE: 4
 112 Phe Ser Tyr Gly Ala Ala Ile Pro Gln Ser Thr Gln Glu Lys Gln
 113 1 5 10 15
 116 <210> SEQ ID NO: 5
 117 <211> LENGTH: 15
 118 <212> TYPE: PRT
 119 <213> ORGANISM: Bacillus sp.
 121 <220> FEATURE:
 122 <221> NAME/KEY: MISC_FEATURE
 123 <222> LOCATION: (12)..(12)
 124 <223> OTHER INFORMATION: Xaa can be any natural amino acid
 126 <400> SEQUENCE: 5
W--> 127 Ser Asp Pro Tyr His Phe Thr Val Asn Ala Ala Xaa Glu Thr Glu 128 1 5 10 15
 131 <210> SEQ_ID NO: 6
 132 <211> LENGTH: 1302
 133 <212> TYPE: DNA
 134 <213> ORGANISM: Citrobacter braakii YH-15
 136 <220> FEATURE:
 137 <221> NAME/KEY: gene
 138 <222> LOCATION: (1)..(1302)
 139 <223> OTHER INFORMATION: phytase gene
 141 <400> SEQUENCE: 6

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142	atgagtacat	tcatcatttcg	tttattaatt	ttttctctct	tatgcgggttc	tttctcaata	60										
144	catgctgaag	agcagaacgg	catgaaactg	gagcgggttg	tgatagtgag	ccgtcatgga	120										
146	gtaagagcac	ctacgaagtt	cactccaata	atgaaaagatg	tcacaccgga	ccaatggcca	180										
148	caatggatg	tgccgttagg	atggctaacg	cctcggtggg	gagaacttgt	ttctgaattt	240										
150	ggtcagtatc	aacgttatg	gttcacaagc	aaaggctctgt	tgaataatca	aacgtgccca	300										
152	tctccagggc	aggttctgt	tattgcagac	acggatcaac	gcacccgtaa	aacgggtgag	360										
154	gcgtttctgg	ctgggttagc	accaaaatgt	caaattcaag	tgcattatca	gaaggatgaa	420										
156	aaaaaaaatg	atccctttt	taatccgtt	aaaatgggaa	aatgttcgtt	taacacattt	480										
158	aaggtaaaa	acgctattct	ggaacggggc	ggaggaaata	ttgaactgtt	tacccaacgc	540										
160	tatcaatctt	catttcggac	cctggaaaat	gttttaattt	tctcacaatc	ggagacatgt	600										
162	aagactacag	agaagtctac	gaaatgcaca	ttaccagagg	ctttaccgtc	tgaatttaag	660										
164	gtaactcctg	acaacgttac	attacctgg	gcctggagtc	tttctccac	gctgactgag	720										
166	atatttctgt	tgcaagaggc	ccaggaaat	ccacaggtag	cctggggcgc	tattacggga	780										
168	aaaaaaaatg	ggagagattt	gttaagtctg	cataacgctc	agtttgatct	tttgc当地	840										
170	actccagaag	ttgcccgtag	tagggccaca	ccatctactcg	atatgataga	cactgc当地	900										
172	ttgacaaatg	gtacaacaga	aaacaggat	ggcataaaat	tacccgtatc	tctgttgttt	960										
174	attgctggtc	atgataccaa	tcttgc当地	ttaagcgggg	ctttagatct	taagtggc当地	1020										
176	ctgcccggc	aacccgataa	tacccctcct	ggtggggagc	ttgtattcga	aaagtggaaa	1080										
178	agaaccagt	ataatacgga	ttgggttcag	gtttcattt	tttatcagac	gctgagagat	1140										
180	atgagggata	ttcaaccgtt	gtcgtagaa	aaacctgctg	gaaaagtta	tttaaaatta	1200										
182	attgc当地	aagagaaaaa	tagtcaggg	atgtgtcgt	taaaaagttt	ttccaggc当地	1260										
184	attaaggaaa	ttcgc当地	agagtgtc	gttacggaa	aa		1302										
187	<210>	SEQ ID NO:	7														
188	<211>	LENGTH:	433														
189	<212>	TYPE:	PRT														
190	<213>	ORGANISM:	Citrobacter braakii YH-15														
192	<220>	FEATURE:															
193	<221>	NAME/KEY:	PEPTIDE														
194	<222>	LOCATION:	(1)..(433)														
195	<223>	OTHER INFORMATION:	phytase														
197	<400>	SEQUENCE:	7														
198	Met	Ser	Thr	Phe	Ile	Ile	Arg	Leu	Leu	Ile	Phe	Ser	Leu	Leu	Cys	Gly	
199	1				5				10						15		
201	Ser	Phe	Ser	Ile	His	Ala	Glu	Glu	Gln	Asn	Gly	Met	Lys	Leu	Glu	Arg	
202					20				25						30		
204	Val	Val	Ile	Val	Ser	Arg	His	Gly	Val	Arg	Ala	Pro	Thr	Lys	Phe	Thr	
205					35				40						45		
207	Pro	Ile	Met	Lys	Asp	Val	Thr	Pro	Asp	Gln	Trp	Pro	Gln	Trp	Asp	Val	
208					50				55						60		
210	Pro	Leu	Gly	Trp	Leu	Thr	Pro	Arg	Gly	Gly	Glu	Leu	Val	Ser	Glu	Leu	
211	65				70				75						80		
213	Gly	Gln	Tyr	Gln	Arg	Leu	Trp	Phe	Thr	Ser	Lys	Gly	Leu	Leu	Asn	Asn	
214					85				90						95		
216	Gln	Thr	Cys	Pro	Ser	Pro	Gly	Gln	Val	Ala	Val	Ile	Ala	Asp	Thr	Asp	
217					100				105						110		
219	Gln	Arg	Thr	Arg	Lys	Thr	Gly	Glu	Ala	Phe	Leu	Ala	Gly	Leu	Ala	Pro	
220					115				120						125		
222	Lys	Cys	Gln	Ile	Gln	Val	His	Tyr	Gln	Lys	Asp	Glu	Glu	Lys	Asn	Asp	
223					130				135						140		

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```

225 Pro Leu Phe Asn Pro Val Lys Met Gly Lys Cys Ser Phe Asn Thr Leu
226 145 150 155 160
228 Lys Val Lys Asn Ala Ile Leu Glu Arg Ala Gly Gly Asn Ile Glu Leu
229 165 170 175
231 Tyr Thr Gln Arg Tyr Gln Ser Ser Phe Arg Thr Leu Glu Asn Val Leu
232 180 185 190
234 Asn Phe Ser Gln Ser Glu Thr Cys Lys Thr Thr Glu Lys Ser Thr Lys
235 195 200 205
237 Cys Thr Leu Pro Glu Ala Leu Pro Ser Glu Phe Lys Val Thr Pro Asp
238 210 215 220
240 Asn Val Ser Leu Pro Gly Ala Trp Ser Leu Ser Ser Thr Leu Thr Glu
241 225 230 235 240
243 Ile Phe Leu Leu Gln Glu Ala Gln Gly Met Pro Gln Val Ala Trp Gly
244 245 250 255
246 Arg Ile Thr Gly Glu Lys Glu Trp Arg Asp Leu Leu Ser Leu His Asn
247 260 265 270
249 Ala Gln Phe Asp Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser Arg
250 275 280 285
252 Ala Thr Pro Leu Leu Asp Met Ile Asp Thr Ala Leu Leu Thr Asn Gly
253 290 295 300
255 Thr Thr Glu Asn Arg Tyr Gly Ile Lys Leu Pro Val Ser Leu Leu Phe
256 305 310 315 320
258 Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Ser Gly Ala Leu Asp
259 325 330 335
261 Leu Lys Trp Ser Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly Gly
262 340 345 350
264 Glu Leu Val Phe Glu Lys Trp Lys Arg Thr Ser Asp Asn Thr Asp Trp
265 355 360 365
267 Val Gln Val Ser Phe Val Tyr Gln Thr Leu Arg Asp Met Arg Asp Ile
268 370 375 380
270 Gln Pro Leu Ser Leu Glu Lys Pro Ala Gly Lys Val Asp Leu Lys Leu
271 385 390 395 400
273 Ile Ala Cys Glu Glu Lys Asn Ser Gln Gly Met Cys Ser Leu Lys Ser
274 405 410 415
276 Phe Ser Arg Leu Ile Lys Glu Ile Arg Val Pro Glu Cys Ala Val Thr
277 420 425 430
279 Glu
282 <210> SEQ ID NO: 8
283 <211> LENGTH: 30
284 <212> TYPE: DNA
285 <213> ORGANISM: Artificial Sequence
287 <220> FEATURE:
288 <223> OTHER INFORMATION: primer for the detection of phytase gene
290 <400> SEQUENCE: 8
291 gargarcaga ayggatgaa actggarcgy

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 10/07/2005
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 1134
Seq#:5; Xaa Pos. 12

VERIFICATION SUMMARY
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L:14 M:270 C: Current Application Number differs, Replaced Current Application No
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:71 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:1080
L:127 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0